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BACTERIAL VIRULENCE GENES

The present invention relates to the identification of genes involved in the virulence of *Actinobacillus pleuropneumoniae*, to the production of attenuated mutant strains
5 of *Actinobacillus pleuropneumoniae*, and to the identification of anti-bacterial agents which target the identified genes and their products.

A. pleuropneumoniae is the causative agent of porcine pleuropneumonia, a highly contagious, respiratory disease of pigs. The disease is often fatal and as a result
10 leads to severe economic loss in the swine producing industry. An obligate parasite of the porcine respiratory tract, the incidence of infection of *A. pleuropneumoniae* has increased in recent years, notably where animals are subjected to intensive breeding conditions. Transmission of the bacterium is by aerosol, or by direct contact with infected pigs.

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Pleuropneumonia can occur in swine of all ages, and there are no known associations with predisposing viral or bacterial infections. *A. pleuropneumoniae* infection may be chronic or acute, with the disease being characterised by increasingly severe pulmonary distress, which progresses rapidly to death, or to a
20 chronic infection resulting in a failure to thrive. A hemorrhagic, necrotic bronchopneumonia with accompanying fibrinous pleuritis is typically observed.

Fifteen different serotypes of *A. pleuropneumoniae* have been identified based on antigenic differences in their capsular polysaccharides, and their production of
25 extracellular toxins. Serotypes 1, 5 and 7 are the most common forms of *A. pleuropneumoniae* infection in the United States, whereas serotypes 1, 2, 5, 7 and 9 predominate in Europe.

Treatment of pigs infected with *A. pleuropneumoniae* usually involves the direct
30 injection of an antibiotic (typically tetracycline). Such a method is however labour intensive, time consuming, and expensive, and can often be of limited use due to the rapid progression of the disease. Evidence from field and experimental studies

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has however shown that infection with *A. pleuropneumoniae* can provide a lifetime protection against subsequent reinfection, thereby suggesting that vaccination might be a feasible alternative to antibiotic therapy. The development of an effective vaccine has so far been hampered by the antigenic diversity of the fifteen different
5 serotypes.

In attempts to produce a vaccine composition, killed, whole cell bacteria were found to provide only serotype-specific protection, but it has been shown that natural infection with a highly virulent serotype can stimulate a strong protective cross-
10 immunity against multiple serotypes [Nielsen, Nord Vet Med. 31: 407-13 (1979); Nielsen, Nord Vet Med. 36: 221-234 (1984); Nielsen, Can J Vet Res. 29: 580-582 (1988); Nielsen, ACTA Vet Scand. 15: 80-89 (1994)]. Certain undefined live attenuated mutants have also shown promise for cross- protection of swine [Inzana
15 *et al*, Infect Immun. 61: 1682-6 (1993); Paltineanu *et al*, In International Pig Veterinary Society, 1992, p.214; Utrera *et al*, In International Pig Veterinary Society, 1992, p.213] but because of the uncertainties associated with vaccines comprising bacterial strains having such undefined spontaneous mutations, there exists a need in the art for the rational construction of live attenuated strains which will safely stimulate protective immunity against homologous, and preferably heterologous
20 *Actinobacillus pleuropneumoniae* serotypes. There also exists a need to identify the genes involved in *A. pleuropneumoniae* virulence, to facilitate the development of methods for identifying anti-bacterial agents which target those genes and/or their products.

25 Published International patent application WO 00/61724 (Pharmacia & Upjohn) describes the use of signature tagged mutagenesis (STM) to identify genes responsible for the virulence of gram-negative bacteria. The development of vaccines containing attenuated bacteria is also discussed. The work is also described in Fuller *et al*, Microbial Pathogenesis [2000] vol. 26; pp.39-51.

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In the STM technique, a plurality of different bacterial strains, each of which carries a random mutation in its genome, is produced by means of transposon integration.

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The inserted transposons carry different DNA signature tags, which allows individual mutants to be differentiated from one other. The tags each comprise a variable central region flanked by invariant "arms", the latter of which allow the variable central portion to be amplified by PCR. Multiple tagged mutant strains are collected
5 in microtiter dishes, and then combined to form an "inoculum pool" for animal infection.

At an appropriate time after infection, bacteria are isolated from the infected animal, and are combined to form a "recovered pool." The tags in the recovered pool and the tags in the inoculum pool are separately amplified, labelled, and used to probe
10 filters arrayed with all the different tags from the mutants in the inoculum. Mutant strains with attenuated virulence are generally those which cannot be recovered from the infected animal, i.e. strains with tags that give hybridization signals when probed with tags from the inoculum pool, but not when probed with tags from the recovered pool. The advantage of STM is that a large number of insertional mutant
15 strains can be simultaneously screened in a single animal for loss of bacterial virulence. STM is more fully described in e.g. WO 96/17951.

After considerable research, the present inventors have provided improved methods and means for identifying genes involved in *A. pleuropneumoniae* virulence. This
20 has led to the identification of a new family of "virulence genes" the members of which each comprise a nucleotide sequence which is selected from any one of those defined by SEQ ID NO: 1-56. As used herein, the term "virulence genes" refers to genes of a bacterium whose correct function is involved in, e.g. required for the establishment and/or maintenance of an infection in a host animal. Virulence genes
25 and their products, which may be polynucleotides (e.g. rRNA) and/or polypeptides, are thus involved in the pathogenesis of the bacterium, but might not be necessary for its growth *in vitro*.

Mutations in virulence genes can result in an "attenuated bacterium", i.e. one whose
30 ability to establish and/or maintain a bacterial infection in a host animal is reduced, as compared to a corresponding wild-type bacterium of the same strain and serotype. Attenuation of the bacterium may be confirmed by means of its

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administration to a subject animal, where its inability to cause a sustained infection leading to e.g. chronic infection or death may be observed. The non-establishment of symptoms of porcine pleuropneumonia, e.g. of pulmonary distress, hemorrhagic necrotic bronchopneumonia and/or fibrinous pleuritis, may also be used as an index
5 of bacterial attenuation. Attenuated bacteria are of commercial importance in vaccine compositions.

In one aspect, the present invention thus provides an attenuated *Actinobacillus pleuropneumoniae* bacterium.

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In a particular embodiment, the present invention provides an attenuated *Actinobacillus pleuropneumoniae* bacterium having a mutation in a gene which comprises a nucleotide sequence selected from the group consisting of SEQ ID NO.:1-56.

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The mutation may inhibit or prevent the function of the gene, e.g. by reducing the level of its expression (e.g. by reducing transcription and/or translation), and/or by impairing the biological activity of the gene product, e.g. by causing an inactive form of the gene product that is encoded by the mutated gene to be produced. The gene
20 product may be a polynucleotide or polypeptide.

The mutation in the gene may be an insertion, deletion or substitution. It may be located in a region of the gene that encodes a polypeptide, or in a sequence responsible for, or involved in, the control of gene expression, e.g. in a promoter
25 region. Mutations which involve a combination of one or more of insertion, deletion and/or substitution are also contemplated. Attenuated *A. pleuropneumoniae* strains of the present invention likewise include those which have two or more mutations, each of which may be an insertion, a deletion, a substitution, or a combination thereof. Multiple mutations may occur in a single gene, or they may occur in different
30 genes within the same bacterial genome. They may result in an additive or synergistic level of attenuation. Multiple mutations may be prepared by design, or may fortuitously arise as a result of techniques for introducing a single mutation.

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Deletion mutants include those in which all or part of the virulence gene is deleted. In one aspect, the mutation results in the deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least
5 about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of the virulence gene. A deletion may occur in the appropriate nucleotide sequence set forth in SEQ ID NO.:1-56, or it may occur in an adjacent region of the gene, e.g. in an associated control sequence.

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Deletion mutants can be constructed using any technique which is well known to those skilled in the art. One strategy employs counter-selectable markers, and has been used to delete genes in many different bacteria. For details of this technique, reference may be made to e.g. Reyrat *et al*, Infection and Immunity [1998] vol. 66;
15 pp.4011-4017, and Oswald *et al*, FEMS Microbiol Lett [1999] vol. 179; pp.153-160.

The process employs a double selection strategy, in which a plasmid is constructed which encodes both a selectable and a counter-selectable marker, with flanking DNA sequences being derived from both sides of the desired deletion site in the
20 bacterial genome. The selectable marker is used to select for bacteria in which the plasmid has integrated into the genome in the appropriate location and manner. The counter-selectable marker is then used to select for that small percentage of bacteria which spontaneously eliminate the integrated plasmid. A fraction of those resultant bacteria will contain the desired deletion, with no foreign DNA remaining.

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In another technique for achieving a deletion, the *cre-lox* system is used for site specific recombination of DNA. The system consists of 34 base pair *lox* sequences that are recognised by a bacterial *cre* recombinase. If the *lox* sites are introduced into the genomic DNA in an appropriate orientation, a sequence which is flanked by
30 the *lox* sites can be excised by expression of the *cre* recombinase, one copy of the *lox* site being retained. Using standard recombination techniques, it is possible to delete a sequence of interest in the *A. pleuropneumoniae* genome and to replace

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it with a selectable marker (e.g. a gene encoding kanamycin resistance) which is flanked by *lox* sites. Transient expression of the *cre* recombinase (e.g. from an electroporated suicide (non-replicating) plasmid containing the *cre* gene under the control of a promoter which functions in *A. pleuropneumoniae*) will then result in
5 efficient elimination of the *lox* flanked marker. This process results in a bacterial mutant containing the desired deletion, and one copy of the *lox* sequence.

In another approach to providing a deletion, a target sequence in the *A. pleuropneumoniae* genome can be deleted (replaced) with a marker gene, e.g. a
10 green fluorescent protein (GFP), β -galactosidase or luciferase. DNA segments flanking a desired deletion are prepared by PCR and cloned into a suicide vector for *A. pleuropneumoniae*. An expression cassette, containing a promoter active in *A. pleuropneumoniae* and operably linked to the appropriate marker gene, is then cloned between the flanking sequences. The plasmid is introduced into wild-type
15 bacteria and mutants which both incorporate and express the marker gene are isolated and examined for a desired recombination event (replacement of the wild-type gene with the marker gene).

As for insertion mutants, these include genes in which a stop codon is inserted into
20 an open reading frame (ORF) upstream (5') of the native, i.e. endogenous stop signal. A truncated, inactive form of the (polypeptide) virulence gene product may thus be expressed by the gene. Insertions which cause a frame-shift are likewise contemplated for the production of inactive products. Mutated virulence genes of *A. pleuropneumoniae* will also include those in which a transposon has been inserted
25 into a protein-coding or regulatory sequence of the gene. Attenuated bacteria produced by the STM technique are insertional mutants in which a virulence gene has been rendered non-functional by insertion of a transposon sequence, e.g. Tn10.

Because insertional mutants, e.g. those generated by STM, will still contain all of the
30 genetic information required for bacterial virulence, there is a risk that they could revert to a pathogenic state, e.g. by spontaneous deletion of the inserted sequence. Accordingly, when preparing a vaccine or other therapeutic composition, based on

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an insertional mutant, e.g. one identified by STM, it may be desirable to take the information obtained from that STM-derived strain, i.e. the identification of the disrupted virulence gene, and then recreate a mutant in which some, most, or all of that virulence gene has instead been deleted. This should preclude the possibility
5 that the bacterium will revert to a virulent state, thereby to cause pathology, rather than prophylactic protection of a host animal to which it is administered.

In a related aspect, the present invention provides a composition containing the attenuated *A. pleuropneumoniae* bacterium according to the first aspect of the
10 invention. The composition may be an immunogenic composition, i.e. one which is capable of eliciting an antibody response in a host animal to which it is administered. The composition may be a therapeutic (e.g. prophylactic) composition. It may be a vaccine, preferably one whose administration to an animal confers a degree of protection against subsequent infection with serotypes and strains of *A.*
15 *pleuropneumoniae* different from that/those which is/are present in the vaccine itself (cross-protection). The invention further provides for the use of an attenuated *A. pleuropneumoniae* bacterium of the first aspect of the invention for the manufacture of a medicament (e.g. vaccine) for preventing or alleviating an infection of an animal with *A. pleuropneumoniae* and/or for preventing or alleviating symptoms associated
20 with such infection, e.g. for the prophylactic protection of swine against porcine pleuropneumonia.

In order for an attenuated bacterium to be effective in a vaccine composition, the (one or more) mutation(s) in the virulence gene(s) should be significant enough to
25 prevent the pathogen from evoking severe clinical symptoms, but insignificant enough to allow a limited replication and growth of the bacteria in the host animal, thereby to elicit appropriate defence mechanisms resulting in immunological memory. Mutations in genes which are required for (as distinct from merely involved in) virulence are preferred.

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Compositions of the invention may contain a plurality of different attenuated *A. pleuropneumoniae* bacteria, e.g. bacteria having different mutations in the same

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virulence gene, and/or bacteria having similar, or different, mutations in two or more different genes. While it is possible for an avirulent (attenuated) bacterium of the present invention to be administered alone, it is preferably administered in a solid or liquid composition containing one or more suitable adjuvants, diluents, carriers, vehicles and/or excipients, as discussed elsewhere herein. Compositions according to, and for use in the present invention, may thus comprise one or more of these substances, which should be pharmacologically "acceptable", in the sense of being both compatible with the attenuated bacterium, and not deleterious to the animal to be immunized. Additional substances are preferably both sterile and pyrogen free.

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Examples of adjuvants which may be used in the present invention include oil-based adjuvants such as Freund's Complete Adjuvant and Freund's Incomplete Adjuvant, mycolate-based adjuvants (e.g. trehalose dimycolate), bacterial lipopolysaccharide (LPS), peptidoglycans (e.g. mureins, mucopeptides, or glycoproteins such as N-Opaca, muramyl dipeptide [MDP], or MDP analogs), proteoglycans (e.g. those extracted from *Klebsiella pneumoniae*), streptococcal preparations (e.g. OK432), BiostimTM (e.g. O1K2), the "Iscoms" of EP 109 942, EP 180 564 and EP 231 039, aluminum hydroxide, saponin, DEAE-dextran, neutral oils (such as miglyol), vegetable oils (such as arachis oil), liposomes, Pluronic polyols, the Ribi adjuvant system (see e.g. GB-A-2 189 141) and interleukins, particularly those that stimulate cell-mediated immunity. An adjuvant consisting of extracts of *Amycolata*, a genus of bacteria of the order Actinomycetales, has also been described (US 4,877,612). Proprietary adjuvant mixtures are commercially available. The adjuvant to be used will depend, at least in part, on the recipient animal. The amount of adjuvant to be administered will also depend on the type and size of the animal. Optimal dosages may be readily determined by routine methods well known to those skilled in the art.

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As for any diluent(s), carrier(s), vehicle(s) and/or excipient(s), these may be liquid, semisolid, or solid in nature. Any suitable substance known to those skilled in the art may be used. Exemplary substances include polyoxyethylene sorbitan monolaurate, magnesium stearate, methyl and propylhydroxybenzoate, talc, alginates, starches, lactose, sucrose, dextrose, sorbitol, mannitol, gum acacia, calcium phosphate,

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mineral oil, cocoa butter, and oil of theobroma.

The compositions of the invention may be packaged in various forms which maybe convenient for, or adapted to, a particular route of delivery. Therapeutic
5 compositions (e.g. vaccines) may be suitable for administration to a subject animal by for example intravenous, intradermal, intramuscular, intramammary, intraperitoneal and/or subcutaneous injection, and/or by oral, sublingual, nasal, anal or vaginal delivery. The treatment may consist of a single dose, or of a plurality of doses over a period of time. Decisions on administration regimes are well within the
10 ambit of those skilled in the art. The composition may be formulated and packaged as appropriate.

In a further aspect, the present invention provides an isolated polynucleotide encoding a gene product which is naturally involved in (e.g. required for) the
15 virulence of *A. pleuropneumoniae*. The sequence of the polynucleotide is thus found in a virulence gene of *A. pleuropneumoniae*. The invention also provides for a polynucleotide encoding a gene product which is not naturally found in *A. pleuropneumoniae*, but whose expression therein is capable of modulating (e.g. of decreasing) the virulence of that bacterium. Such a polynucleotide may be
20 introduced into the bacterium to cause such expression (e.g. by transformation, transfection or electroporation). Expression may result in an attenuated strain of the bacterium, e.g. for use in a vaccine or other immunogenic composition. Polynucleotides which are not naturally found in *A. pleuropneumoniae* but which are capable of modulating the virulence of that bacterium by their direct interaction with
25 *A. pleuropneumoniae* virulence genes or gene products (rather than by indirect action through their own gene products) are also contemplated.

Any gene product of a polynucleotide according to the present invention may be a polynucleotide (e.g. RNA) or a polypeptide. Polypeptide gene products are herein
30 referred to as "virulence polypeptides", and are involved in/capable of modulating the virulence of *A. pleuropneumoniae*, whether or not they are naturally encoded by the wild-type bacterial genome. Polynucleotide gene products which can affect the

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virulence of *A. pleuropneumoniae* include e.g. antisense RNA and ribozymes. An effect on bacterial virulence may be demonstrated for any gene product by determining the extent to which a strain of the bacterium *A. pleuropneumoniae* which expresses the product can establish and/or maintain an infection in an animal
5 as compared with *A. pleuropneumoniae* of the same strain and serotype which does not express the product.

According to this aspect, the present invention more particularly provides for an isolated polynucleotide comprising (e.g. consisting of): (a) a nucleotide sequence
10 selected from the group consisting of SEQ ID NO.: 1-56 (such sequences are found within the virulence genes of *A. pleuropneumoniae* as identified elsewhere herein); (b) a nucleotide sequence encoding the polypeptide which is encoded by the nucleotide sequence recited in (a); (c) a nucleotide sequence which hybridizes to the nucleotide sequence of (a) and/or (b), or to its complement, under conditions of
15 moderate to high stringency; or (d) a fragment of any one of the nucleotide sequences of (a)-(c), which fragment retains an immunological property and/or a biological activity of the recited nucleotide sequence of (a)-(c). Polynucleotides of the present invention may be DNA or RNA, as described elsewhere herein.

20 Nucleotide sequences of type (b) can be readily identified once an amino acid sequence is derived from the nucleotide sequence of (a), and account is taken of the genetic code.

As to (c), exemplary conditions of moderate stringency include a final wash in a
25 buffer comprising 2xSSC/0.1% SDS, at 35°C to 45°C. Exemplary conditions of high stringency include a final wash in a buffer comprising 0.2xSSC/0.1 % SDS, at 65°C to 75°C. It is understood in the art that conditions of equivalent stringency can be achieved by means of variation of temperature and buffer or of salt concentration. In this regard, reference may be made to Ausubel *et al*, Protocols in Molecular
30 Biology, John Wiley & Sons (1994), pp.6.0.3 to 6.4.10. Modifications in hybridization conditions can be empirically determined or precisely calculated based on length and percentage of guanosine/cytosine (GC) base pairing. Hybridization conditions

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can be calculated as described in Sambrook *et al*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York (1989), pp. 9.47 to 9.51.

- 5 For fragments of type (d), knowledge of the nucleotide sequence according to (a), (b) or (c) makes available to the skilled person every possible fragment of that nucleotide sequence. Fragments may be at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, or at least 50 nucleotides in length. They may be capable of hybridising to the nucleotide sequence of (a), (b) or
10 (c), or to its complement, under conditions of moderate to high stringency, optionally in the presence of competitive nucleic acid, e.g. in the presence of nucleic acid from a cDNA or mRNA library derived from *A. pleuropneumoniae*. The retained immunological property may be an ability of the fragment to be bound specifically by an antibody which binds specifically to the full length nucleotide sequence.
- 15 Binding affinities of at least 10^7 M^{-1} are contemplated. A retained biological activity may be an ability of the fragment to encode a polypeptide which shares a binding capability with the polypeptide encoded by the full length nucleotide sequence, e.g. an ability to bind to one of the ligands to which it naturally binds *in vivo*, or the same antibody.

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- As will be readily apparent to the person of skill in the art, the identification of virulence genes of *Actinobacillus pleuropneumoniae* enables the identification of corresponding (i.e. homologous) genes in other related bacteria, e.g. in other members of the *Pasteurellaceae* family. In isolated form, such gene sequences may
25 be encompassed within the claimed polynucleotides comprising (or consisting of) a nucleotide sequence according to type (c) above. Southern hybridization using the nucleotide sequences of type (a) (or fragments thereof) as probes, can identify such related sequences in genomic, cDNA or mRNA libraries from other bacteria. Alternatively, the use of PCR, with primers comprising the *A. pleuropneumoniae*
30 sequences or fragments thereof, can be equally as effective for identifying virulence genes across species boundaries. As a further alternative (which does not rely on hybridisation but still identifies homologous genes) complementation of an *A.*

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pleuropneumoniae mutant strain with a polynucleotide (e.g. DNA or mRNA) library from another species, can be used to identify genes having the same, or a related biological activity. In short, polynucleotides of the invention, which comprise a nucleotide sequence according to type (c), may be found in, or constitute, virulence genes of other bacteria related to *A. pleuropneumoniae*.

Identification of related virulence genes can lead to the production of an attenuated strain of the other organism by mutation in that gene, and may therefore be used in the production of vaccines and other immunological compositions. In yet further aspects, the present invention thus provides: (1) an attenuated bacterium (e.g. of the *Pasteurellaceae* family) containing a mutation in a gene comprising a nucleotide sequence which is capable of hybridising to any one of the nucleotide sequences defined by SEQ ID NO:1-56, under conditions of moderate to high stringency; (2) a composition (e.g. a vaccine) containing such a bacterium; and (3) the use of such a bacterium for the manufacture of a medicament (e.g. a vaccine) for the therapeutic treatment or prophylactic protection of an animal against infection by the corresponding wild-type bacterium (or a different strain or serotype thereof).

As explained elsewhere herein, polynucleotides of the present invention of types (a)-(d) may be e.g. DNA, RNA, or peptide nucleic acids, as described for example in Corey, TIBTECH 15: 224-229 (1997). DNA sequences include those derived (extracted or amplified) from genomic DNA, or from cDNA, as well as wholly or partially chemically synthesized nucleotide sequences. Amplification may be effected by any method well known to those skilled in the art, e.g. by PCR.

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"Chemically synthesized" as used herein refers to purely chemical, as opposed to enzymatic (e.g. PCR-based) methods for producing polynucleotides. "Wholly" synthesized polynucleotides are those produced entirely by chemical means, and "partially" synthesized polynucleotides include those wherein only portions of the resulting sequence are produced by chemical means.

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The polynucleotides of the invention, or their gene products, may be ribozymes.

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Such polynucleotides may comprise or consist of an (RNA) nucleotide sequence according to type (c) above, i.e. one which is capable of hybridising to any of the nucleotide sequences recited in (a) or (b) under conditions of moderate to high stringency. For a review of ribozyme technology, reference is made to Gibson and
5 Shillito, Mol. Biotech. 7: 125-137 (1997). A ribozyme can be utilized to inhibit the translation of mRNA (e.g. mRNA transcribed from virulence genes) in a sequence specific manner, e.g. by: (i) the hybridization of a complementary RNA sequence in the ribozyme to the target mRNA; and (ii) cleavage of the hybridized target mRNA through nuclease activity inherent to the ribozyme. The polynucleotides of the
10 invention may therefore be used to inhibit the expression of virulence genes of *A. pleuropneumoniae* or of other related e.g. *Pasteurellaceae* bacteria. Ribozymes can be identified by empirical methods, but they may be specifically designed based on accessible sites on the target mRNA, e.g. on the mRNA transcription product of the nucleotide sequences defined by SEQ ID NO:1-56 (see also Bramlage *et al*, Trends
15 in Biotech 16: 434-438 (1998)).

Delivery of ribozymes to target cells, in order to control mRNA translation, may be accomplished using delivery techniques well known to those skilled in the art. Exogenous delivery methods can include the use of targeting liposomes or direct
20 local injection. Endogenous methods include the use of viral vectors and of non-viral plasmids.

Certain polynucleotides of the present invention may also be used to modulate the transcription of virulence genes in *A. pleuropneumoniae*, e.g. by means of
25 oligonucleotide-directed triplet helix formation. For a review of this technique, reference is made to Lavrovsky *et al*, Biochem. Mol. Med. 62: 11-22 (1997). Triplet helix formation is accomplished using sequence specific oligonucleotides which hybridize to double stranded DNA in the major groove (as defined in the Watson-Crick model). Hybridization of such sequence specific oligonucleotides can
30 thereafter modulate the activity of DNA-binding proteins, including, for example, transcription factors and polymerases. Preferred target sequences for hybridization include transcriptional regulatory regions that modulate the expression of virulence

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genes. Oligonucleotides which are capable of triplet helix formation are also useful for site-specific covalent modification of target DNA sequences in virulence genes. Oligonucleotides useful for covalent modification are coupled to DNA damaging agents as described for example in Lavrovsky, *et al*, Biochem. Mol. Med. 62: 11-22
5 (1997).

In yet another aspect, the present invention provides a vector comprising a polynucleotide according to the present invention. The vector may be DNA or RNA in nature. It may contain one or more control sequences operably linked to the
10 polynucleotide, in order to promote its transcription, and optionally enable its translation, in a suitable host cell under appropriate conditions. Vectors may be plasmids, or viral vectors. They may be capable of autonomous replication. Control sequences may be endogenous (i.e. found within the wild-type bacterium from which the polynucleotide of the invention is derived, e.g. *A. pleuropneumoniae*) or they
15 may be exogenous (e.g. a control sequence found in a related bacterium, e.g. in another member of the *Pasteurellaceae* family). Control sequences include *inter alia* promoters and transcription terminators.

Host cells containing (e.g. transformed, transfected, or electroporated with) a
20 polynucleotide or vector of the present invention are further contemplated. Such host cells may be prokaryotic or eukaryotic in nature, either stably or transiently transformed, transfected, or electroporated with a polynucleotide or vector of the present invention, in a manner which permits the transcription of the polynucleotide, and optionally enables translation of the resultant mRNA. Host cells of the invention
25 include bacterial, yeast, fungal, invertebrate, and mammalian cells. Viruses containing a polynucleotide or vector of the present invention are also contemplated.

Host cells of the present invention may be useful in methods for the large scale production of virulence polypeptides (where the polynucleotide of the invention
30 encodes a polypeptide sequence). The cells are grown in a suitable culture medium under favourable conditions, and the desired polypeptides are isolated from the cells, or from the medium in which the cells are grown, by any purification technique

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well known to those skilled in the art, e.g. by capture on an affinity column. Such cells may be a valuable source of immunogen for the development of antibodies which specifically bind to the virulence polypeptide. Any suitable host cell may be used for the expression of a polynucleotide according to the present invention.

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For this and other purposes, polynucleotides of the present invention may be manipulated using standard techniques well within the ambit of those skilled in the art, e.g. the techniques described in Sambrook *et al*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York (1989). By way of example, the polynucleotides of the invention may be amplified and cloned by e.g. PCR, e.g. using genomic DNA, cDNA or mRNA as a template. For ease of inserting the cloned sequence into vectors, e.g. expression vectors, PCR primers may be chosen so that the PCR-amplified sequence has a restriction enzyme site at the 5' end which precedes the initiation codon ATG, and a restriction enzyme site at the 3' end after the termination codon TAG, TGA, or TAA. If desirable, the codons in the cloned sequence may be changed, without changing the amino acids, according to the codon preference of an intended host cell, e.g. *E. coli*, as described by Grosjean and Fiers, Guide, 18: 199-209 (1982) and Konigsberg and Godson, Proc. Natl. Acad. Sci. (USA), 80: 687-691 (1983). Optimization of codon usage may lead to an increase in the expression of the gene product when produced in that host.

If a virulence polypeptide is to be produced extracellularly, e.g. in the periplasm of a host bacterium, or in the culture medium surrounding a host cell, then the polynucleotide of the present invention may be cloned without its initiation codon, and placed into an expression vector behind an appropriate signal sequence. A number of signal sequences from both prokaryotes and eukaryotes are known to function in the secretion of recombinant proteins. During the protein secretion process, the signal peptide may be removed by a signal peptidase to yield the mature protein.

To simplify the purification of virulence polypeptides, a purification tag may be added

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to the 5' and/or 3' end of the polypeptide encoding sequence. Commonly used purification tags include a stretch of six histidine residues (US Patent Nos. 5,284,933 and 5,310,663), a streptavidin-affinity tag described by Schmidt and Skerra, Protein Engineering, 6: 109-122 (1993), a FLAG peptide (Hopp et al., Biotechnology, 6: 12051210 (1988)), glutathione S-transferase (Smith and Johnson, Gene, 67: 31-40 (1988)), and thioredoxin (LaVallie et al., BioTechnology, 11: 187-193 (1993)). To remove these tags, a proteolytic cleavage recognition site may be inserted at the fusion junction. Commonly used proteases are factor Xa, thrombin, and enterokinase.

- 10 In a further aspect, the present invention provides a method of producing a virulence polypeptide encoded by a polynucleotide of the invention. The method may comprise the steps of: (i) culturing a host cell according to the present invention under conditions which permit the expression of the polypeptide; and (ii) recovering and optionally isolating the expressed polypeptide from the host cell, or from its
- 15 surrounding medium. Identification of the polynucleotides of the present invention readily makes available their encoded polypeptides, so such polypeptides can alternatively be chemically synthesised.

Polypeptides encoded by polynucleotides of the present invention (and variants of such polypeptides) are a further aspect of the invention. Such polypeptides are "virulence polypeptides", as discussed elsewhere herein. Compositions containing such polypeptides are further contemplated, and these include vaccines and other immunogenic compositions. Such compositions may contain one or more adjuvants, carriers, diluents, vehicles or excipients, as discussed elsewhere herein.

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Variants include biologically and/or immunologically active fragments of the polypeptide encoded by a polynucleotide of the invention, e.g. fragments of the polypeptide encoded by the polynucleotide sequence defined in any one of SEQ ID NO.:1-56, fusions of the polypeptides or fragments thereof with e.g. heterologous

30 polypeptides (thereby to produce chimeras), and analogs of the polypeptides, e.g. polypeptides in which one or more amino acids has been deleted, replaced or added: (i) without loss of one or more of the biological activities and/or

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immunological characteristics specific for the polypeptide; or (ii) with specific disablement of a particular biological activity of the polypeptide. Replacement may occur using conservative amino acids.

- 5 Virulence polypeptides having an additional methionine residue at position -1 are contemplated, as are virulence polypeptides having additional methionine and lysine residues at positions -2 and -1. Variants of these types are particularly useful for recombinant protein production in bacterial cell types. The invention also embraces variants having additional amino acid residues which result from the use of specific
10 expression systems. For example, use of commercially available vectors that express a desired polypeptide as a fusion protein with glutathione-S-transferase (GST) provide the desired polypeptide having an additional glycine residue at position -1 after cleavage of the GST component from the desired polypeptide. Variants of polypeptides of the present invention also include those in which a leader
15 or signal sequence has been removed, e.g. a mature form.

Variant polypeptides include those which have at least about 99%, at least about 95%, at least about 90%, at least about 85%, at least about 80%, at least about 75%, at least about 70%, at least about 65%, at least about 60%, at least about
20 55%, and at least about 50% sequence identity and/or homology with a virulence polypeptide encoded by a nucleotide sequence as defined in any one of SEQ ID NO.:1-56. Percentage "identity" of an amino acid sequence is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in the virulence polypeptide, after aligning both sequences and
25 introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Percent "homology" of an amino acid sequence with respect to a virulence polypeptide encoded by any one of SEQ ID NO:1-56 refers to the percentage of amino acid residues in the candidate sequence that are identical with the residues
30 in the virulence polypeptide after aligning the two sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and also considering any conservative substitutions as part of the sequence identity.

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By conservative substitution is meant exchange of one amino acid for an amino acid of the same type, the types being as follows:

Aliphatic Non-polar :	G A P I L V
5 Polar-uncharged sulphur :	C M
Polar-uncharged hydroxyl:	S T
Polar-charged acidic:	D E N Q
Polar-charged basic:	K R H
Aromatic:	F W Y

10

In a still further aspect, the present invention extends to antibodies which specifically recognize the polynucleotides or polypeptides of the present invention. Antibodies may be monoclonal or polyclonal antibodies. They include chimeric antibodies, e.g. humanized antibodies, e.g. complementary determining region (CDR)-grafted

15 antibodies, as well as fragments of antibodies (which may be chimeric) e.g. Fab, F(ab')₂, Fd and single chain antibodies. They also include compounds having CDR sequences which specifically recognize a polynucleotide or polypeptide of the present invention. The invention also provides anti-idiotypic antibodies which specifically bind to antibodies of the present invention.

20

The term "specific for" indicates that the variable regions of the antibodies of the invention exclusively recognize a target polypeptide or polynucleotide (i.e. they are able to distinguish a single polypeptide or polynucleotide from related polypeptides or polynucleotides). Binding affinities of at least about 10^7 M^{-1} , at least about 10^8 M^{-1} , or at least about 10^9 M^{-1} are contemplated. That is not to say that the antibodies

25 will not also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practised by those skilled in the art. For a

30 comprehensive discussion of such assays, reference may be made to Harlow et al. (Eds), Antibodies. A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring

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Harbor, NY (1988), Chapter 6.

According to a still further aspect of the present invention, materials and methods are provided for identifying an anti-bacterial agent which is capable of modulating the function of an *A. pleuropneumoniae* virulence gene identified by the present invention, or of a homologous gene in a related species. Agents which are capable of modulating the function of such virulence genes are likewise contemplated *per se*. More particularly, methods of the present invention include screening potential agents for their ability to interfere with the expression and/or biological activity in a host bacterium of the gene products encoded by the nucleotide sequences set forth in any one of SEQ ID NO:1-56. Agents that interfere with the expression of virulence gene products include (but are not limited to) anti-sense polynucleotides and ribozymes containing nucleotide sequences which are homologous to any one of the nucleotide sequences of SEQ ID NO:1-56 (such that they bind to its complement). The invention further embraces methods of modulating the transcription of such virulence genes through the use of oligonucleotide-directed triplet helix formation.

Compositions containing an anti-bacterial agent identified in accordance with the present invention are a still further aspect of the present invention, in addition to a method of treating an animal suffering from a *Pasteurellaceae* (e.g. an *A. pleuropneumoniae*) infection by administration of such an anti-bacterial agent or composition. The invention also embraces the use of such an agent or composition for the manufacture of a medicament for the treatment of a *Pasteurellaceae* infection, e.g. an *A. pleuropneumoniae* infection and/or porcine pleuropneumonia.

Agents that interfere with the function of virulence genes encompass: (i) non-functional variants of the virulence gene products which may be capable of out-competing the wild-type product for its physiological binding sites; and (ii) binding partners of the virulence gene products, which sequester and optionally destroy said products. Agents also include allosteric enzyme inhibitors, in the case where the virulence gene product is an enzyme.

- 20 -

Inhibitory agents may be identified by means of high throughput screening assays using the polynucleotides of the present invention or their encoded products (which may be RNA polynucleotides or polypeptides). Where the screen employs polypeptide gene products having enzymatic activity, assays are established which are based on that activity, and potential agents screened for an ability to modulate (e.g. inhibit) the activity. For virulence gene products which exert their function by interacting with a polypeptide or nucleic acid, binding assays are established to measure such interaction, and potential agents are screened for an ability to modulate, e.g. to inhibit the interaction.

10

In one example of a binding assay, the virulence gene product is immobilized on a solid support, and an interaction with a (physiological) binding partner is assessed in the presence and absence of a putative inhibitor compound. In another example, interaction between the virulence gene product and its binding partner is assessed in a solution assay, both in the presence and absence of a putative inhibitor compound. In both assays, an inhibitor is identified as a compound that decreases binding between the virulence gene product and its binding partner. Assays for use when the virulence gene product and its binding partner are both polypeptides include variations of the di-hybrid assay, wherein an inhibitor of protein/protein interaction is identified by detection of a positive signal in a transformed or transfected host cell, as described for example in published International patent application WO 95/20652.

25 Candidate inhibitors contemplated for use in the methods of the present invention include compounds selected from libraries of potential inhibitors. A number of different libraries can be used as a source of small molecule modulators, including: (1) chemical libraries; (2) natural product libraries; and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

30 Chemical libraries consist of structural analogs of known compounds. Natural product libraries are collections of microorganisms, animals, plants, or marine organisms which are used to create mixtures for screening by: (i) fermentation and

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extraction of broths from soil, plant or marine microorganisms; or (ii) extraction of plants or marine organisms. Natural product libraries are further discussed in e.g. Science 282: 63-68 (1998). As for combinatorial libraries, these are composed of large numbers of peptides, oligonucleotides, or organic compounds as a mixture.

- 5 They are relatively easy to prepare by traditional automated synthesis methods, PCR, cloning, or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. For a review of combinatorial chemistry libraries, reference may be made to Myers, Curr. Opin. Biotechnol. 8: 701-707 (1997).
- 10 Still other candidate inhibitors, which are contemplated for use in the methods of the invention, may be specifically designed. These include soluble forms of the binding partners of virulence polypeptides. The term "binding partners" as used herein encompasses antibodies (although in certain embodiments these are excluded) including fragments and derivatives thereof, and modified compounds comprising
- 15 antibody domains that specifically bind to the target gene product.

When a polypeptide binding partner for a virulence gene product is not known, assays that identify physiological, or non-physiological and hence sequestering binding partners may be employed, e.g. assays using affinity columns on which the

20 virulence gene product is immobilised. Alternatively, binding interactions between polypeptides may be identified using the yeast two-hybrid system as described in Fields and Song, Nature, 340: 245-246 (1989), and Fields and Sternglanz, Trends in Genetics, 10: 286-292 (1994). Other assays which may be used to search for agents that bind to a polypeptide virulence gene product include that described in

25 US Patent No. 5,585,277, which relies on the principle that proteins generally exist as a mixture of folded and unfolded states, and continually alternate between the two states. When a test ligand binds to the folded form of a target virulence polypeptide, the target protein molecule bound by the ligand remains in its folded state. Thus, the folded target protein is present to a greater extent in the presence

30 of a test ligand which binds the target protein, than in the absence of a ligand. Binding of the ligand to the target protein can be determined by any method which distinguishes between the folded and unfolded states of the target protein. The

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function of the target protein need not be known in order for this assay to be performed. Virtually any agent can be assessed by this method as a test ligand, including, but not limited to metals, polypeptides, including proteins, lipids, polysaccharides, polynucleotides and small organic molecules.

5

Another method for identifying ligands of a virulence gene polypeptide is that described in Wieboldt *et al*, Anal. Chem., 69: 1683-1691 (1997). That technique screens combinatorial libraries of 20-30 agents at a time in solution phase for binding to the target virulence polypeptide. Agents that bind to the target are
10 separated from other smaller library components by centrifugal ultra-filtration. The specifically selected molecules that are retained on the filter are subsequently liberated from the target protein and analysed, e.g. by HPLC and pneumatically assisted electrospray (ion spray) ionization MS. This procedure selects library components with the greatest affinity for the target protein, and is particularly useful
15 for libraries of small molecules.

Binding agents identified by the initial screens maybe evaluated for their effect on virulence *in vivo*. Agents that interfere with bacterial virulence can prevent the establishment of an infection, or reverse the outcome of an infection once it is
20 established. Binding agents may be included in compositions containing pharmaceutically acceptable adjuvants, excipients, diluents, carriers or vehicles, as described elsewhere herein.

Numerous additional aspects and advantages of the invention will now become
25 apparent to those skilled in the art upon consideration of the following detailed description of the invention which describes presently prepared embodiments thereof.

30 EXPERIMENT 1

A. Materials and Methods

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1. Bacterial strains and growth conditions

A spontaneously nalidixic acid-resistant derivative of the virulent *Actinobacillus pleuropneumoniae* serotype 1 strain 4074 was selected using conventional methods and designated 4074 Nal^R. The virulence of this strain was verified by passage in pigs. *A. pleuropneumoniae* strains were propagated at 37°C with 5% CO₂ on brain-heart infusion (BHI) plates supplemented with 10% Levinthal's base (BHI_L), or at 37°C in Colombia broth with 5µg/ml β-nicotinamide adenine dinucleotide (NAD) and 11mM CaCl₂.

The *E. coli* strains used in this study were: S17 λ pir [*recA thi pro hsdR* M⁺ RP4::2-Tc::Mu::Km Tn7 lysogenized with λ pir phage] as described in Miller and Mekalanos (1988) J. Bacteriol. 170, pp.2575-2583; CC118 λ pir [*Δ(are-leu) araD Δ lacX74 galE galK phoA20 thi-1 rpsE rpoB argE recA1* lysogenized with λ pir phage] as described in de Lorenzo *et al*, (1990) J. Bacteriol. 172, pp. 6657-6667; and XL1-Blue (*recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac [F' proAB lac^R ZΔM15 Tn10 (Tet^r)]*). *E. coli* strains were maintained in Luria-Bertani (LB) medium with appropriate antibiotics used at the following concentrations: ampicillin 100µg/ml; kanamycin 100µg/ml; nalidixic acid 20µg/ml; tetracycline 10µg/ml.

2. DNA manipulations, amplification, labelling, and hybridisation of tags

Chromosomal DNA was isolated from *A. pleuropneumoniae* using a QIAamp mini DNA kit (Qiagen) according to the manufacturer's instructions. Plasmid DNA was isolated from *E. coli* using a Qiagen plasmid midi kit, again according to the manufacturer's instructions. DNA manipulation was performed according to standard techniques as described in Sambrook *et al*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York (1989). Probes for southern blots were labelled with [digoxigenin (DIG)-11]-dUTP using a PCR DIG Probe Synthesis Kit (Roche) as described by the manufacturer. Amplification and labelling of DNA signature-tags was performed as described in

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Hensel *et al* (1995) Science 269 pp.400-403. Tags were initially amplified from genomic DNA by means of PCR using the following primers:

P6 (5'-CGACTACAACCTCAAGCT-3')

5

P7 (5'-CGACCATTCTAACCAAGC-3')

The amplified tags were purified on a 2% Nusieve GTG agarose gel and radiolabelled with [³²P]-dCTP in a second PCR, again using P6 and P7. The cycling conditions for both PCRs were as follows: denaturation and enzyme activation
10 12min at 95°C, followed by 20 cycles of: 95°C for 30s, 50°C for 45s and 72°C for 10s. Reactions were performed using 1 unit of AmpliTaq Gold (Perkin-Elmer) polymerase in a Perkin-Elmer 2400 thermocycler. Prior to use, the invariant flanking DNA was separated from the variable signature-tag by digestion with *HindIII* for 18h at 37°C.

15

For colony blots, *E. coli* S17 λ pir strains harbouring each of the pLOF/TAG 1-48 plasmids were grown to mid-exponential phase and 100 μ l of each culture was transferred to the wells of a microtitre dish. Bacteria were transferred from the microtitre dish to a nylon membrane (Hybond N) using a replica plater (Sigma) and
20 the inoculated membrane placed on the surface of a dried LB agar plate containing ampicillin (100 μ g/ml). After overnight growth at 37°C, the membranes were treated with 1.5 M NaCl, 0.5 M NaOH for 10min. DNA was fixed to the membrane by microwaving at maximum power for 30s and bacterial debris removed by washing in 2XSSC. Pre-hybridisation and hybridisation were performed at 65°C in Rapid-hyb
25 buffer (Amersham) for 1h and overnight, respectively. Blots were washed according to standard procedures. To identify potentially attenuated mutants, hybridisation signals on a blot probed with labelled tags prepared from the input pool (inoculum) were compared to identical blots hybridised with labelled tags prepared from the corresponding output pools from at least two different animals.

30

3. Construction of DNA signature-tags and pLOF/TAG 1-48

- 25 -

Double-stranded DNA signature tags were obtained by PCR amplification of the variable oligonucleotide pool RT1 (Hensel *et al*, 1995 Science 269 pp.400-403) using the following primers:

5 P3SAL (5'-CGCCATGTCGACCATTCTAACCAAGCTT-3')
 P5SAL (5'-CGCCTAGTCGACTACAACCTCAAGCTT-3')

each of which contains recognition sites for the restriction endonuclease *Sall* at its 5' terminus. To facilitate the cloning of the signature-tags in plasmid pLOF/Km, the
10 plasmid was modified to incorporate a unique *Sall* site. This was done by annealing the following complementary oligonucleotides:

 SALTOP (5'-GTCGACCCT-3') and
 SALBTM (5'-GTCGACAGG-3').

15 to give a double-stranded linker containing a *Sall* site flanked by *SfiI*-compatible ends. Plasmid pLOF/Km was digested with *SfiI*, treated with calf intestinal alkaline phosphatase (CIAP), and ligated to the phosphorylated double-stranded linker to give plasmid pLOF/Sal. The PCR-amplified double-stranded DNA signature-tags
20 were digested with *Sall*, gel purified, and cloned into the *Sall*- digested, CIAP-treated, pLOF/Sal to generate a library of uniquely tagged pLOF/TAG plasmids.

Individual transformants in *E. coli* strain CC118 λ pir were screened by colony blot hybridisation with their corresponding [³²P]-dCTP-labelled tags to identify 100 tags
25 that amplified and labelled efficiently. These tags were then tested for an absence of cross-hybridisation and 48 plasmids (pLOF/TAG1-48) were selected for further use.

4. Construction of the signature-tagged mutant bank

30

The 48 signature-tagged mini-Tn10 transposons carried on plasmids pLOF/TAG 1-48 were separately introduced into *A. pleuropneumoniae* by conjugation. *A.*

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pleuropneumoniae strain 4074 Nal^R and *E. coli* S17 λ pir harbouring each of the pLOF/TAG 1-48 plasmids were grown overnight at 37°C to the stationary phase of growth. Bacteria were harvested by centrifugation for 15 minutes at 3,000 rpm and washed twice with 10mM MgSO₄. Approximately equal numbers of *A.*
5 *pleuropneumoniae* recipient and *E. coli* donor cells were mixed, concentrated, and spread onto 0.22 μ M filters. Filters were placed onto BHI_L plates containing 1mM IPTG and incubated at 37°C with 5% CO₂ for 5 hours. Thereafter, the bacteria were removed into 5ml sterile PBS and aliquots plated onto BHI_L plates supplemented with nalidixic acid (20 μ g/ml) and kanamycin (100 μ g/ml). Four separate matings were
10 performed for each of the 48 signature-tagged mini-Tn10 transposons. Transconjugant mutants were screened for susceptibility to ampicillin, thereby to eliminate strains carrying co-integrants of the suicide vector, inserted into the chromosome. In total 2064 transposon mutants from 48 individual matings were isolated and arranged into 43 pools of 48 mutants. Mutants were stored in 1.5ml
15 cryotubes with 15% glycerol at -80°C.

5. Infection studies

Individual strains in each pool of 48 *A. pleuropneumoniae* signature-tagged mutants
20 were grown separately until the mid-exponential phase of growth. At an OD₆₀₀ of approximately 0.3, the individual mutant strains were combined and the pooled culture was diluted in HEPES to approximately 2 x 10⁶ cfu/ml. Large White Cross piglets, of 6-10 weeks of age and determined to be *A. pleuropneumoniae* free by bacteriological and serological analyses, were inoculated intra-tracheally with 3ml
25 of the diluted culture. The number of cfu in the inoculum was verified by viable counts after plating serial dilutions of the inoculum on selective BHI_L. Each mutant pool was used to infect at least two animals.

At approximately 24h post-infection, surviving animals were euthanised and the
30 lungs were removed. Surviving bacteria were recovered from infected lungs by either: (i) extensive lavage with Hanks buffered saline solution (HBSS); or (ii) homogenising the lungs in 500ml HBSS. Aliquots of the bacterial suspension were

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plated on selective media, and following growth overnight at 7°C with 5% CO₂, approximately 10,000 colonies were pooled (the "output pool") and total chromosomal DNA was prepared.

5 6. *Competitive indices*

To determine the *in vivo* competitive index (CI) of individual STM mutants, mutant and wild-type bacteria were grown in Colombia broth with 5µg/ml NAD and 11 mM CaCl₂ to an OD₆₀₀ of 0.3. The cultures were then combined to give equal numbers
10 of mutant and wild-type organisms, diluted to 2x10⁶ cfu/ml, and inoculated intra-tracheally into at least two animals. The ratio of mutant to wild-type bacteria in the inoculum was verified by viable counts after plating serial dilutions of the inoculum in parallel on BHI_L + 20µg/ml nalidixic acid (mutant and wild-type), and BHI_L + 20µg/ml nalidixic acid + 100µg/ml kanamycin (mutant only). Approximately 24h post-
15 infection, surviving animals were euthanised and the lungs were removed. The lungs were homogenised in 500ml HBSS and aliquots were plated on selective media (see above) to recover surviving bacteria. The *in vivo* CI was calculated as the output ratio of mutant to wild-type organisms divided by the input ratio of mutant to wild-type organisms. To determine *in vitro* CIs, mutant and wild-type organisms were
20 grown to mid-exponential phase, mixed in equal numbers, and the combined culture incubated, with agitation, at 37°C for a further 3h. Samples were taken at regular intervals, diluted, and plated on selective BHI_L as before, and the *in vitro* CI was calculated as described above.

25 7. *Virulence gene identification and DNA sequencing*

To identify the *in vivo* attenuating lesions, DNA flanking the site of transposon insertion was cloned or amplified by inverse PCR. For cloning, chromosomal DNA was digested with a panel of restriction enzymes, separated by agarose gel
30 electrophoresis, transferred to a nylon membrane, and probed in a Southern blot with a DIG-labelled probe specific for the Tn10 kanamycin gene. Suitably sized fragments hybridising to the probe were excised from a gel, purified and cloned into

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appropriately digested pBR322. Transformants in *E. coli* strain XL1-Blue were selected on LB agar containing 100µg/ml kanamycin.

To facilitate sequencing with the Tn10 specific oligonucleotide primer:

5

BS401 (5'-GACAAGATGTGTATCCACC-3')

the cloned insert was further sub-cloned into plasmid pBCKS (Stratagene). Inverse PCR amplification of DNA flanking the site of transposon insertion was performed
10 as described in Fuller, (2000) Microb. Pathog. 29, pp.25-38: chromosomal DNA was digested with *SspI* (which cuts once in the transposon), diluted to 150 ng/ml, and self-ligated for 15min using the Rapid DNA Ligation Kit (Roche). The ligated DNA was then amplified using the primer pairs BS401 + TEF48, and BS401 + TEF62 (Fuller, 2000 Microb. Pathog. 29, pp.25-38). Reaction conditions for inverse PCR
15 were as previously described (Fuller, 2000 Microb. Pathog. 29, pp.25-38). The resultant amplicons were purified following agarose gel electrophoresis using a QIAQUICK gel extraction kit (Qiagen). DNA sequencing reactions were performed using the BigDye terminator cycle sequencing kit (Perkin-Elmer). Sequences from each of the attenuated mutants were used to query the non-redundant public DNA
20 and protein databases using the BLAST set of similarity search programs (Altschul *et al* 1990 J. Mol Biol. 15, pp.403-410).

B. Results and Discussion

25 1. *Generation of signature-tagged mutants of A. pleuropneumoniae.*

The plasmid pLOF/Km, which is functional in *A. pleuropneumoniae*, was modified to accept signature-tags by the insertion of a unique *SaI* site in the mini-*Tn10* element. PCR amplified random signature-tags were cloned into the *SaI* site, and
30 a bank of approximately 30,000 tagged plasmids in *E. coli* CC118 λ pir was obtained. A subset of these transformants was screened by colony blot with their corresponding radiolabelled tags, and signature-tagged plasmids with strong

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hybridisation signals were selected. Plasmids with cross-hybridising tags were eliminated, and a pool of 48 unique signature-tagged plasmids was assembled. These plasmids (pLOF/TAG 1-48) were transformed into *E. coli* S17 λ pir, and independently transferred to *A. pleuropneumoniae* strain 4074 Nal^R by conjugation.

5

Following the elimination of ampicillin-resistant plasmid cointegrants (0.5-1%), 2064 transposon mutants from 48 individual matings were isolated, and then arranged into 43 pools of 48 mutants. Southern blot analysis of ten randomly chosen exconjugants with a mini-Tn10-specific probe confirmed single, random insertion of the tagged transposon (data not shown). However, subsequent sequence analysis of attenuated clones revealed that mini-Tn10 insertion in *A. pleuropneumoniae* was not entirely random.

10

2. Signature-tagged screen of *A. pleuropneumoniae* mutants in pigs

15

Signature-tagged *A. pleuropneumoniae* mutants were screened using a porcine intra-tracheal infection model to identify genes involved in virulence. Bacteria were instilled directly into the trachea as previous studies have shown that aerosol particles produced by sneezing are small enough to penetrate into the lower respiratory tract, obviating the need for colonisation of the upper respiratory tract (Kaltreider HB. in Immunologic and infectious diseases in the lung. (1976) pp. 73-97, Kirkpatrick & Reynolds (Eds) Marcel Dekker, New York).

20

A range of experimental factors including the infecting dose, and the method of recovery were investigated before we could reproducibly recover the majority of individual mutants following *in vivo* selection in the porcine host. Using challenge doses of 10^3 , 10^4 , or 10^5 cfu, for example, there was a poor correlation between the infecting dose and the appearance of clinical or morphological signs of disease. Moreover, when different pigs were infected with the same pool, the hybridisation patterns of the post-passage pool suggested that different clones were missing after passage of a given pool through different animals (data not shown). This inconsistency was overcome by increasing the challenge dose to 10^6 - 10^7 cfu/pig.

25

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- 30 -

In an earlier STM study of *A. pleuropneumoniae* infection in pigs [Fuller, 2000 Microb. Pathog. 29, pp.39-51], bacteria were recovered by lung lavage following experimental infection. However, this method was found to be unreliable, yielding essentially random recovery of individual signature tags. In contrast, we observed consistent recovery of viable bacteria following homogenisation of the entire lung in HBSS. Optimisation of these two crucial parameters resulted in the recovery of the majority of individual clones (>90%, 20-48h post infection), with excellent reproducibility between animals (see Figure 1; compare A and B).

In total, 2064 transposon mutants (43 pools of 48 mutants) were screened for attenuation *in vivo*, each pool being inoculated into at least two different animals. Surviving bacteria were recovered by homogenisation of lungs in sterile HBSS. This initial screen identified 550 mutants present in the input pool but missing or significantly reduced in the output pools. These potentially attenuated mutants were reassembled into new pools and each new pool was used to infect a further two animals. Following this second screen, 105/410 mutants were found to be consistently absent from the output pools, and these were retained for further analysis.

3. *Identification and analysis of A. pleuropneumoniae virulence genes.*

The nucleotide sequence of the DNA flanking the site of transposon insertion was obtained for each of the 105 attenuated mutants as described, and used to search the GenBank databases for homologous genes. The results of this analysis are shown in Table 1, with the genes assigned to one of five functional categories: cell surface, transport, metabolism, stress responses, and regulation. Insertions in genes encoding proteins with no significant homology to proteins in the databases, or homologous to proteins or predicted proteins of unknown function, are categorised as "unknown". The 105 attenuated mutants contained transposon insertions in 53 individual genes and a number of hotspots for Tn10 insertion were identified. In

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particular, seven identical insertions were independently isolated in the putative *rfbP* gene (*Tn* insertion at codon 444), 3 of 4 insertions in the *A. pleuropneumoniae fur* gene were located at codon 128. Interestingly, the DNA sequences flanking the 3 hotspots which were identified in this study are neither similar to each other, nor to the consensus sequence for *Tn10* insertion into *A. pleuropneumoniae* that has been previously been identified (Fuller et al (2000) Microb. Pathog. 29, pp.25-38).

(i) Cell surface

10 Mutations in capsule and lipopolysaccharide (LPS) genes are known to attenuate *A. pleuropneumoniae* (Rioux *et al.*, Can. J Microbiol. 45: pgs1017-1026, 1999) (Rioux *et al.*, Microb Pathog 28: pgs 279-289, 2000; Ward *et al.*, Infect Immun 66: pgs 3326-3336, 1998). Mutant 9C2 contains a transposon insertion in the *cpxC* gene that encodes a protein involved in capsule export in *A. pleuropneumoniae* 15 (Ward and Inzana, 1997). This mutant was used as a control (known attenuated) strain the *in vivo* CI experiments. Five genes involved in the synthesis of O-antigen of *A. pleuropneumoniae* serotype 1 were identified in this STM screen. Mutants with inserts in genes 9 (mutant 10B11), 12 (mutant 25B7), 15 (mutant 15A9), 17 (mutant 12D5), and 18 (mutant 21B8) of the O-antigen operon (Labrie *et al.*, 2002, J. Endotox Res. 8: 27-38) were all attenuated. Another mutant, 9B7, has the transposon insertion 20 bases upstream of the *A. pleuropneumoniae galU* gene that encodes a protein involved in synthesis of the LPS core. Mutation of *galU* was previously shown to attenuate *A. pleuropneumoniae* (Rioux *et al.*, 1999). Finally, mutant 26A9 contains an insertion in a gene homologous to *lcbB*, a putative 25 bifunctional polymerase implicated in capsule or LPS biosynthesis in *N. meningitidis* serogroup L.

Strain 4D4 contains a transposon insertion in a gene encoding a putative lipoprotein. Strain 4D4 shows greatest homology to an unknown protein from *P. multocida*, but 30 it is similar to lipoproteins and putative lipoproteins of *H. influenzae* and *H. somnus* [Theisen (1993) Infect Immun 61: 1793-1798]. *H. somnus* LppB binds Congo red dye (a structural analogue of heme) and has been suggested to be a virulence

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factor, but this has not been formally proven [Theisen (1993) Infect Immun 61: 1793-1798]. Finally, strain 17A4 contains an insertion in an ORF with homology to the P2 porin protein of *H. influenzae* [Duim et al (1993) Microb. Pathog. 14, pp. 451-462]. The P2 protein constitutes approximately one half of the total outer membrane
5 protein of *H. influenzae* and represents an important target of the immune response to non-typeable *H. influenzae* infection. [Yi et al (1997) Infect. Immun. 65, 150-155].

(ii) Metabolism

10 Strain 10B12 contains a transposon insertion in an ADP-ribose pyrophosphatase (*adpP*) gene homologue. Regulation of cellular levels of ADP-ribose (ADP-ribose is derived from NAD) is important in preventing non-enzymatic ADP-ribosylation of proteins. The *E. coli*, ADP-ribose pyrophosphatase catalyses the hydrolysis of ADP-ribose to ribose-5-P and AMP, compounds that can be recycled as part of nucleotide
15 metabolism [Gabelli et al (2001) Nat Struct. Biol. 8, pp. 467-472].

Strain 10A11 carries an insertion in an argininosuccinate synthase, *argG*, gene homologue. Argininosuccinate synthase catalyses the conversion of citrulline and aspartate into argininosuccinate, linking the urea cycle and the citric acid cycle via
20 the so-called aspartate-argininosuccinate shunt. The aspartate-argininosuccinate shunt provides a metabolic link between the pathways by which amino groups and the carbon skeletons of amino acids are processed. (Glansdorff (1996) Biosynthesis of arginine and polyamines. In *Escherichia coli* and *Salmonella* (Vol. 1) (Neidhardt, F.C. et al., eds), pp. 408-433, ASM Press).

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In strain 33C7, the attenuating lesion was found to occur in a gene homologous to *H. influenzae atpA*, encoding the F_1 alpha subunit of F_1F_0 ATP synthase. ATP synthase is responsible for utilising the proton electrochemical gradient across the cytoplasmic membrane for ATP synthesis in cells growing aerobically or
30 anaerobically. All eight subunits of the bacterial enzyme are encoded by the *atp* operon. In *P. multocida* the *atpA* gene is flanked by *atpH* and *atpG*, and while the gene order in *A. pleuropneumoniae* is unknown, both *atpH* and *atpG* have been

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implicated previously in the pathogenesis of *A. pleuropneumoniae* infection [Fuller (2000) Microb. Pathog. 29, pp.39-51].

In strain 0A7, the transposon has inactivated the *pntB* gene, encoding the beta
5 subunit of NAD(P) transhydrogenase. Transhydrogenase is an integral membrane
protein composed of two subunits, α and β , organised as an $\alpha_2\beta_2$ tetramer.
Transhydrogenase couples the redox reaction between NAD(H) and NADP(H) to the
translocation of protons across the inner membrane (Penfound & Foster (1996)
Biosynthesis and recycling of NAD. In *Escherichia coli* and *Salmonella* (Vol. 1)
10 (Neidhardt, F.C. et al., eds), pp. 408-433, ASM Press). It plays a key role in energy
metabolism, biosynthesis and detoxification.

In strain 19D5, the transposon has inserted in the *A. pleuropneumoniae mrp* gene.
The partial *A. pleuropneumoniae mrp* gene sequences available are highly
15 homologous to *mrp* genes from *H. influenzae* and *E. coli*. In *H. influenzae*, the *mrp*
gene has been implicated in the biosynthesis of the Gala(1-4) β Gal component of
LPS, while in *E. coli* mutations in *mrp* affect the synthesis of thiamine [High et al
(1996) FEMS Microbiol. Lett. 145, pp.325-331; Petersen (1996) J. Bacteriol. 178, pp.
5676-5682]. In *A. pleuropneumoniae*, the *mrp* gene is located approximately 1kb
20 upstream from the *apxIVA* gene, encoding the *in vivo*-induced RTX toxin, ApxIV
[Schaller (1999) Microbiology 145: 2105-2116].

Strain 29B11 contains a transposon insertion in a *napB* gene homologue, encoding
the smaller, dihaem cytochrome c, subunit of heterodimeric periplasmic nitrate
25 reductase (NAP). In *H. influenzae* (and *Pseudomonas sp*) NAP is the sole nitrate
reductase and may function to support anaerobic growth in the presence of nitrate
[Brige (2001) Biochem. J. 356, pp. 851-858; Fleischmann (1995) Science 269, pp.
496-512; Bedzyk (1999) J Bacteriol 181: 2802-2806]. In *E. coli* the situation is more
complex with two membrane bound respiratory nitrate reductases in addition to NAP
30 [Moreno-Vivian (1999) J Bacteriol 181: 6573-6584]. There is evidence to suggest
that NAP is a dissimilatory enzyme used for redox balancing. In addition, NAP has
been suggested to play a role in adaptation to anaerobic metabolism after transition

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from aerobic conditions, the utilisation of alternate reductants, or even as a self-defense mechanism forming high nitrite levels to inhibit the growth of competing bacteria [Moreno-Vivian (1999) J Bacteriol 181: 6573-6584]. Consistent with a role in anaerobic adaptation, transcription of the *Salmonella typhimurium napB* gene is
5 induced, in an Fnr-dependent manner, in cells exposed to anaerobic conditions [Wei and Miller (1999) J. Bacteriol. 181, pp. 6092-6097].

Strain 17B8, contains an insertion in a gene homologous to *H. influenzae ccmH*, required for the assembly of C-type cytochromes, including NAP, in enteric bacteria
10 [Thony-Meyer (1995) J. Bacteriol. 177, pp. 4321-4326; Kranz (1998) Mol Microbiol 29, pp. 383-396]. CcmH is encoded by the final gene of the *ccm* operon and with CcmF and CcmG is believed to catalyse the reduction of disulphide bonds in the cytochrome c apoprotein and to facilitate haem attachment [Kranz (1998) Mol Microbiol 29, pp. 383-396]. While in *E. coli* the *nap* and *ccm* operons are contiguous
15 and may be cotranscribed [Grove (1996) Mol Microbiol 19, pp. 467-481] they are located at separate loci in both *H. influenzae* and *P. multocida* [Fleischmann (1995) Science 269, pp. 496-512; May (2001) Proc Natl Acad Sci USA 98, pp. 3460-3465].

Strain 4B9 contains a transposon insertion in a *moaA* gene homologue. In *E. coli* the
20 *moaA-E* genes are required for the synthesis of molybdopterin from GTP [Rivers (1993) Mol Microbiol 8: 1071-1081]. Molybdopterin (molybdopterin guanine dinucleotide) is the principal cofactor found in prokaryotic molybdoproteins including periplasmic nitrate reductase. Expression of the *moa* genes is induced by anaerobiosis [Anderson (2000) J. Bacteriol. 182, pp. 7035-7043] and *Salmonella*
25 *typhi moaA* mutants are impaired in their ability to replicate within epithelial cells [Contreras (1997) Microbiology 143, pp. 2665-2672].

Mutant 29B12 contains an insertion in the *A. pleuropneumoniae recR* gene homologue. The RecR protein is involved in the RecF pathway of recombinatorial
30 DNA repair: *recR* mutants are deficient at filling in daughter strand gaps in newly synthesised DNA [Kuzminov (1999) Microbiol Mol Biol Rev 63, pp. 751-813]. Mutations in *recR* delay induction of the SOS response in *E. coli* and such mutants

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are sensitive to UV-irradiation and mitomycin C [Keller (2001) Mutat Res 486, pp. 21-29].

In strain 26A10, the transposon has inserted in a gene with extensive homology to
5 *thrC* of *H. influenzae*. The *thrC* gene encodes threonine synthase, the final enzyme
in the biosynthetic pathway leading to the production of threonine (Patte (1996)
Biosynthesis of threonine and lysine. In *Escherichia coli* and *Salmonella* (Vol. 1)
(Neidhardt, F.C. et al., eds), pp. 408-433, ASM Press). Mutations in a
Streptococcus pneumoniae thrC homologue attenuate the virulence of this organism
10 in a murine model of pneumoniae [Lau (2001) Mol Microbiol 40, pp. 555-571].

In strain 26D12, the transposon has inactivated a GMP synthase, *guaA*, gene
homologue. GMP synthase catalyses the synthesis of GMP from XMP as part of the
purine biosynthetic pathway. Mutations in the *guaBA* operon attenuate the virulence
15 of a variety of enteric pathogens including *E. coli*, *S. flexneri*, and *S. typhi*, and a
 Δ *guaBA S. typhi* derivative shows promise as a live attenuated vector [Wang (2001)
Infect Immun 69, pp. 4734-4741; Noriega (1996) Infect Immun 64, 3055-3061;
Russo (1996) Mol Microbiol 22, pp. 217-229]. Moreover, previous STM screens in
Streptococcus agalactiae and *P. multocida* have implicated *guaA* and *guaB*,
20 respectively, in growth *in vivo* and in pathogenesis [Jones (2000) Mol Microbiol 37,
pp. 1444-1455; Fuller (2000) Microb Pathog 29, pp. 39-51].

Mutant 27A12 contains a transposon insertion in a gene previously identified in *A.*
pleuropneumoniae as *tonB* (Tonpitak et al., Infect Immun 68: 1164-1170 2000)
25 (now referred to as *tonB1*). This gene is found immediately upstream of, and is be
co-transcribed with, *exbB*, *exbD*, and the transferrin binding protein (*tbp*) genes. In
contrast, strain 0F6 contains a transposon insertion in an ORF encoding a protein
with homology to TonB proteins from *P. multocida* and *Haemophilus sp.* (now
designated *tonB2*). Moreover, sequence analysis of the region upstream from the
30 transposon insertion in 0F6 revealed the presence of distinct *exbB* and *exbD* gene
homologues, suggesting that *A. pleuropneumoniae*, in common with other bacterial
pathogens including *V. cholerae* and *P. aeruginosa*, possesses two independent

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TonB systems (Occhino *et al.*, Mol Microbiol 29: 1493-1507 1998; Zhao and Poole, FEMS Microbiol Lett 184: 127-132 2000).

Strain 35D11 contains an insertion in a gene homologous to *H. influenzae dsbA*.

- 5 DsbA is a small periplasmic protein and a member of the thioredoxin superfamily [Debarbieux (1999) Cell 99, pp.117-119]. Mutations in *dsbA* are pleiotropic, affecting the production of a variety of translocated proteins including bacterial virulence factors, components of type III secretion machinery, and c-type cytochromes including NAP [Yu and Kroll (1999) Microbes Infect 1, pp. 1221-1228]. Mutations in
- 10 *dsbA* and *dsbB* have been implicated in the virulence of *Shigella flexneri* [Yu (1998) Infect Immun 66, 3909-3917] and *P. multocida* [Fuller (2000) Microb Pathog 29, pp. 25-38], respectively.

- In strain 26C3, the transposon has inactivated a glutamyl-tRNA reductase, *hemA*,
- 15 gene homologue while in strain 26D5 the transposon has inserted in a putative uroporphyrinogen decarboxylase *uroD/hemE* gene homologue. Glutamyl-tRNA reductase catalyses the reduction of glutamate to glutamate 1-semialdehyde, the first committed step unique to the formation of δ -aminolevulinate (ALA) from glutamate. Downstream from ALA formation, uroporphyrinogen decarboxylase
- 20 catalyses the decarboxylation of uroporphyrinogen III to yield coproporphyrinogen, the first step in the conversion of uroporphyrinogen III to protoheme via protoporphyrin IX. Hemes, including protoheme, are key components of the electron transfer apparatus and in addition play important roles as enzyme prosthetic groups in mineral nutrition and oxidative catalysis (Beale, Biosynthesis of hemes. In
- 25 *Escherichia coli and Salmonella* (Vol. 1) (Neidhardt, F.C. et al., eds), pp. 408-433, ASM Press).

- In strain 15A11, the transposon has inserted into a gene homologous to *P. multocida visC*. The protein encoded by *visC* encodes a putative monooxygenase
- 30 belonging to the UbiH/CoQ6 family. UbiH is required for the biosynthesis of ubiquinone [Nakahigashi (1992) J. Bacteriol. 174, pp. 7352-7359], a prenylated benzoquinone that functions in the respiratory electron chain in the plasma

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membrane of prokaryotes. Ubiquinone and protoheme also function in the formation of disulfide bonds in periplasmic proteins by facilitating the oxidation of DsbA by DsbB [Kobayashi (1997) Proc Natl Acad Sci USA 94, pp. 11857-11862].

- 5 Strain 29A10 contains a transposon insertion in a gene homologous to *prfC* of *H. influenzae*. The *prfC* gene encodes peptide chain release factor 3 (RF3), a GTPase that in the presence of GTP catalyses the removal of RF1 and RF2 from the ribosome after translation termination [Freistroffer (1997) EMBO J 16 4126-4133]. The efficient recycling of RF1 and RF2 by RF3-GTP, although dispensable for
10 viability in prokaryotes, is required for maximum growth rate [Kisselev (2000) Trends Biochem Sci 25, pp. 561-566].

In strains 26A6 and 33B7 the transposon has inserted in genes with homology to the *tmmH* family of tRNA/rRNA methyltransferases. The interrupted ORF in strain 26A3
15 shows greatest homology to *H. influenzae yibK*, while that in strain 33B7 shows most similarity to *yjfh* of *H. influenzae*.

(iii) Regulation

- 20 Virulence genes involved in environmental sensing and coordinate regulation were identified in this screen. The *A. pleuropneumoniae* homologue of the ferric uptake regulator, *fur*, was found to be inactivated in strain 6C12. Fur or Fur-like proteins have been shown to regulate virulence factor expression in a variety of pathogens including *E. coli* (Shiga-like toxin), *Corynebacterium diphtheriae* (diphtheria toxin), and
25 *Pseudomonas aeruginosa* (exotoxin A) [Prince (1991) Mol. Microbiol 5 pp.2823-2831; Schmitt (1991) Infect Immun 59, pp. 1899-1904; Calderwood (1987) J. Bacteriol 169, pp. 4759-4764]. Strains 21D3 and 19B10 contain transposon insertions in the *A. pleuropneumoniae rpoE* and upstream *mclA* (*rseA*) gene homologues, respectively. The *rpoE* encoded sigma factor, σ^E /Sigma-24, is a
30 member of the extracytoplasmic function subfamily of sigma factors that function as effector molecules in response to extracytoplasmic stimuli including heat shock and oxidative stress [Raina (1995) EMBO J 14, pp. 1043-1055; Rouviere (1995) EMBO

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J. 14 1032-1042; Ades (1999) *Genes Dev* 13, pp. 2449-2461; Dartigalongue (2001) *J Biol Chem* 276, pp. 20866 - 20875]. In *S. typhimurium*, σ^E is an important determinant of virulence and immunogenicity [Humphreys (1999) *Infect Immun* 67, pp. 1560-1568]. MclA (RseA) is an inner membrane protein that acts as a σ^E -
5 specific anti- σ factor. MclA (RseA) is rapidly degraded in response to extracytoplasmic stress resulting in increased σ^E concentration and initiation of the stress response [Ades (1999) *Genes Dev* 13, pp. 2449-2461]. Finally, insertions in the *A. pleuropneumoniae* quorum sensing *luxS* homologue (strain 26D3) were observed to attenuate *A. pleuropneumoniae* virulence. Recently, the *E. coli luxS*
10 homologue has been implicated in the control of intestinal colonisation factors encoded by the locus of enterocyte effacement pathogenicity island in both EHEC and EPEC [Sperandio (2001) *J Bacteriol* 183, pp. 5187-5197; Sperandio (1999) *Proc Natl Acad Sci USA* 96, pp. 15196 - 15201].

15 (iv) Transport

The *A. pleuropneumoniae* gene *aopA* is inactivated in strain 23C9. The *aopA* gene encodes a 48 kDa immunogenic outer membrane protein that is common to all serotypes of *A. pleuropneumoniae* tested [Cruz (1996) *Infect Immun* 64 pp. 83-90].
20 Interestingly, AopA is highly homologous (75% identity, 84% similarity) to Nqr1 of *H. influenzae* (NqrA of *Vibrio alginolyticus*), encoding the alpha chain of the sodium-translocating NADH-ubiquinone oxidoreductase (NQR) complex [Hayashi (1996) *FEBS Lett* 381 pp. 174-176; Beattie (1994) *FEBS Lett* 356 pp. 333-338]. The NQR enzyme is a respiration-linked Na^+ pump establishing an electrochemical gradient
25 of sodium ions across the membrane. The resultant sodium motive force can be used for solute transport, ATP synthesis, and flagellar rotation. This alternative energy coupling of sodium ions rather than protons enables the bacteria to maintain a cytoplasmic pH near neutrality in an alkaline environment. The NQR enzyme has been most extensively studied in *V. alginolyticus* where it is thought to be involved
30 in pH and ion homeostasis [Beattie (1994) *FEBS Lett* 356 pp. 333-338; Unemoto (1993) *J. Bioenerg Biomembr* 25 pp. 385-391]. In *Vibrio cholerae*, the NQR complex has been implicated in the regulation of virulence factor expression via its effects on

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ToxT expression [Hase (1999) Proc Natl Acad Sci USA 96 pp. 3183-3187].

Components of several different putative ABC transport systems were identified as necessary for virulence of *A. pleuropneumoniae*. ABC transport systems are
5 involved in the transport (uptake or efflux) of a diverse array of macromolecules across the cytoplasmic membrane of bacteria and eukaryotes. These systems usually consist of three basic parts: one or two ATPases, one or two integral membrane proteins and a substrate-specific binding protein. Strains 13B12, 0C5, 19D1, and 24A4 contain transposon insertions in the ATPase component of ABC
10 transporters. The gene inactivated in strain 0C5 encodes a protein with significant homology to MglA of prokaryotic galactose transporters (Richarme *et al.*, J Biol Chem 268: 9473-9437, 1993). The *in vivo* CI of this mutant indicates limited availability of certain sugars within the respiratory tract environment. The interrupted ORFs in strains 19D1 and 24A4 are homologous to hypothetical ATPases from
15 transport systems of unknown specificity in *P. multocida* (PM1728 and PM0996, respectively). In strain 20D10, the transposon has inactivated a gene with extensive homology to *znuA* of *H. ducreyi* and *pzp1* of *H. influenzae* (Lewis *et al.*, Infect Immun 67: 5060-5068, 1999; Lu *et al.*, J Biol Chem 272: 29033-29038 1997 and FEMS Microbiol Lett 165: 129-137 1998). ZnuA (PZP1) is a periplasmic zinc-binding protein
20 that plays a key role in zinc uptake. Inactivation of the *znuA* gene in *H. ducreyi* caused a significant decrease in virulence in the rabbit model for experimental chancroid (Lewis *et al.*, Infect Immun 67: 5060-5068, 1999). In strain 0D6 the transposon has inserted in a gene encoding a protein with homology to putative integral membrane proteins from *P. multocida* (PM0997) and *N. meningitidis*
25 (NMB0549). In *P. multocida* PM0997 is located immediately upstream from the ATPase inactivated in strain 24A4 suggesting that they are part of the same transport system (May *et al.*, Proc Natl Acad Sci U S A 98: 3460-3465 2001). This gene was also identified by Fuller *et al.* (Fuller *et al.*, Microb Pathog 29: 39-51 2000) as *apvD*, the predicted product of which shows homology with the macrolide-specific
30 ABC-type efflux protein MacA (Kobayashi *et al.*, J Bacteriol 183: 5639-5644 2001). In mutant 9D10, the disrupted gene sequence encodes a protein with homology to CorC which mediates both influx and efflux of magnesium as well as cobalt efflux

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(Gibson et al., Mol Microbiol., 5: pgs 2753-2762,[1991]).

(v) Stress

5 In strain 13A3, the transposon has inserted in a *dnaJ* gene homologue. DnaJ is an essential component of bacterial Hsp70 chaperone systems where it functions as a co-chaperone, providing substrate specificity to its Hsp70 partner, DnaK [Rudiger (2001) EMBO J 20 pp. 1042-1050]. In addition to their fundamental roles in protein folding and translocation, DnaK/DnaJ constitute the primary stress-sensing and
10 transduction system of the *E. coli* heat shock response [Tomoyasu (1998) Mol Microbiol 30 pp.567-581] where they modulate the induction of the heat shock response by altering the stability of the heat shock sigma factor σ^{32} . Significantly, mutations in DnaK have previously been shown to attenuate *A. pleuropneumoniae* virulence and to decrease the survival of *Brucella suis* in human macrophage-like
15 cell lines [Fuller (2000) Microb Pathog 29 pp. 39-51; Kohler (1996) Mol Microbiol 20 pp. 701-712].

Strain 26B6 contains an insertion in a *htpG* gene homologue. HtpG is a heat shock-induced molecular chaperone that, in *E. coli*, contributes to the correct folding of
20 cytoplasmic proteins in mildly stressed cells [Thomas (2000) Mol Microbiol 36 1360-1370]. HtpG does not appear to associate stably with partner proteins and little is known about its mechanism of action. It has been suggested that HtpG serves as a holder chaperone, transiently maintaining a subset of de novo synthesised proteins in a conformation that is accessible to DnaK/DnaJ [Freeman (1996) EMBO
25 J 15 pp.2969-2979].

Strain 13D8 contains a transposon insertion in a *lon* gene homologue. Lon (also called protease La) is a heat shock-inducible, ATP-dependent serine protease that plays a major role in the elimination of abnormally folded proteins [Gottesman (1996)
30 Annu Rev Genet 30 465-506; Suzuki (1997) Trend Biochem Sci 22 pp.118-123]. In addition to its demonstrated role as a stress response protease, Lon also functions as a pleiotropic regulator of gene expression by degrading unstable regulatory

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proteins including RcsA, a positive regulator of capsule synthesis [Keenleyside (1992) J Bacteriol 174 pp. 8-16] and Sula, an inhibitor of cell division and component of the *E. coli* SOS response [Mizusawa (1983) Proc Natl Acad Sci USA 80 pp. 358-362]. Recent studies in *Brucella abortus* have demonstrated that Lon is
5 required for survival in murine macrophages and wild-type virulence in the mouse model of infection [Robertson (2000) Mol Microbiol 35: 577-588].

Strain 13C1 carries a transposon insertion in a *prc* gene homologue. Prc is a periplasmic protease whose natural substrates appear to be membrane proteins
10 including TonB [Gottesman (1996) Annu Rev Genet 30 pp.465-506]. It has been speculated that Prc functions as a chaperone involved in the folding and turnover of proteins in the periplasmic space [Bass (1996) J Bacteriol 178 pp.1154-1161].